

AMENDMENTS TO THE SPECIFICATION

Paragraph bridging pages 10 and 11, r place with the following paragraph:

"Sequence identity" as referred to herein in connection with nucleotide sequences refers to the value obtained when assessed using ClustalW (Thompson et al., 1994, Nucl. Acids Res., 22, p4673-4680) with the following parameters:

Pairwise alignment parameters - Method: accurate,
Matrix: IUB, Gap open penalty: 15.00, Gap extension penalty: 6.66;
Multiple alignment parameters - Matrix: IUB, Gap open penalty: 15.00, % identity for delay: 30, Negative matrix: no, Gap extension penalty: 6.66, DNA transitions weighting: 0.5.

In connection with amino acid sequences, "sequence identity" refers to sequences which have the stated value when assessed using ClustalW (Thompson et al., 1994, supra) with the following parameters:

Pairwise alignment parameters - Method: accurate,
Matrix: PAM, Gap open penalty: 10.00, Gap extension penalty: 0.10;
Multiple alignment parameters - Matrix: PAM, Gap open penalty: 10.00, % identity for delay: 30, Penalize end gaps: on, Gap separation distance: 0, Negative matrix: no, Gap extension penalty: 0.20, Residue-specific gap penalties: on, Hydrophilic gap penalties: on, Hydrophilic residues: GPSNDQEKR (SEQ ID NO:1). Sequence identity at a particular residue is intended to include identical residues which have simply been derivatized.

Please replace Table 1, page 23, with the following Table 1.

Table 1. Details of recombinant monomer/peptide combinations used.

Monomer ID	Allele	Peptide sequence
A2/gag (6)	A*0201	SLYNTVATL ⁵ (9)(SEQ ID NO:2)
B7/EBV	B*0702	RPPIFIRRL (10)(SEQ ID NO:3)
B8/HCV (8)	B*0801	HSK ⁵ KKKDEL (11)(SEQ ID NO 4)
A11/nef	A*1101	QVPLRPMTYK (12)(SEQ ID NO 5)
A11/pol	A*1101	AIFQSSMTK (13)(SEQ ID NO:6)
A11/EBV1	A*1101	IVTDFSVIK (SEQ ID NO:7)
A11/EBV2	A*1104	AVFDRKSVIK (14)(SEQ ID NO:8)